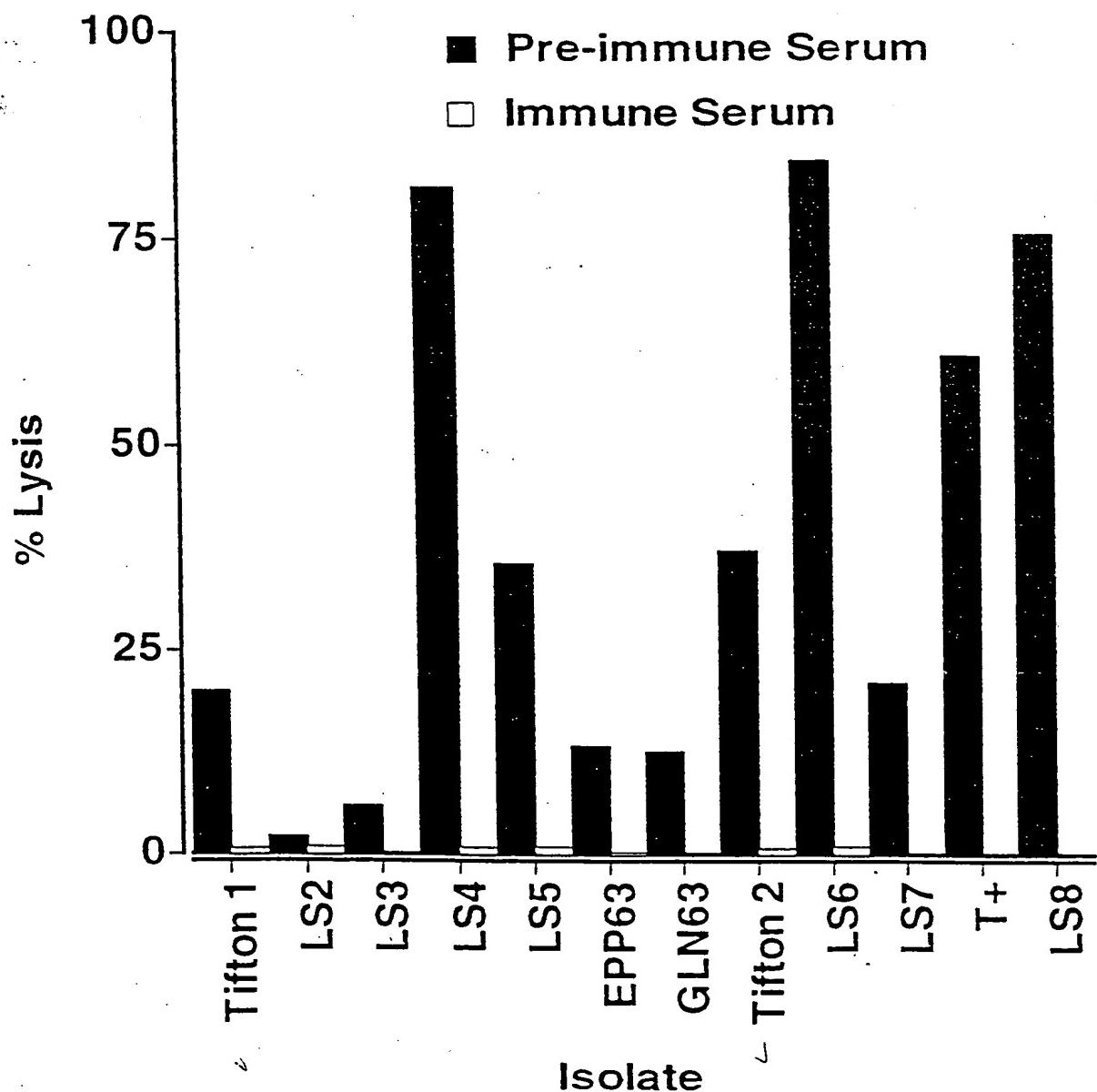


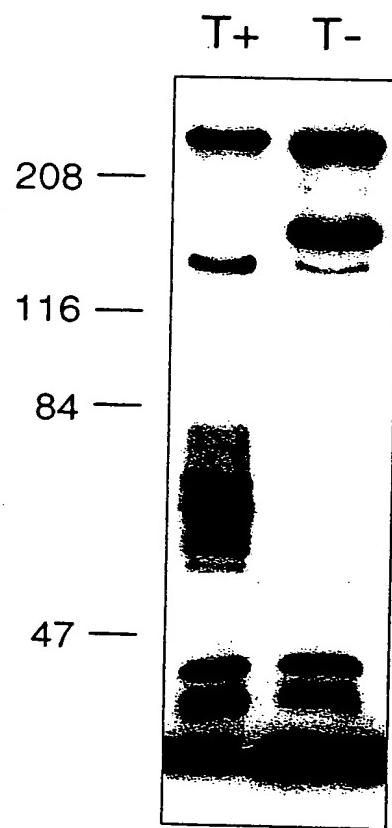
#5

FIG. 1



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FIG. 2



# FIG 3-1

## Appendix A update-July 1999

Bases 1-1200

Amino acids 1-400

1 ATGTCCAATATAAATGTAATTAAATCTAATATTCAAGCAGGCTTGAATTCAACAAAGTCT	60
1 M S N I N V I K S N I Q A G L N S T K S	20
61 GGATTAAGGGAAATCTTACTTGCTATTCCAAAGATTATGATCGCAAAAGGTGGACT	120
21 G L K N L Y L A I P K D Y D P Q K G G T	40
121 TTAAATGATTTATTAAAGCTGCTGATGAATTAGGTATTGCTCGTTAGCAGAAGAGCCT	180
41 L N D F I K A A D E L G I A R L A E E P	60
181 AATCACACTGAAACAGCAAAAAATCTGTTGACACAGTAAATCAGTTCTCTCTCACA	240
61 N H T E T A K K S V D T V N Q F L S L T	80
241 CAAACTGGTATTGCTATTCCTGCAACAAAATTAGAAAAGTTCTAACAAAACATTCTACC	300
81 Q T G I A I S A T K L E K F L Q K H S T	100
301 AATAAGTTAGCAAAGGGTTAGACAGTGTAGAAAATATTGATCGTAAATTAGTAAAGCA	360
101 N K L A K G L D S V E N I D R K L G K A	120
361 AGTAATGTATTATCACATTAAGCTTTGGGCACTGCATTAGCGGGTATAGAACTT	420
121 S N V L S T L S S F L G T A L A G I E L	140
421 GATTCTTAATCAAAAAGGTGATGCTGCACCTGATGCTTGGCTAAAGCTAGTATTGAC	480
141 D S L I K K G D A A P D A L A K A S I D	160
481 TTGATTAATGAGATAATTGGTAATCTATCTCAGAGTACTCAAACGATTGAAGCATTCT	540
161 L I N E I I G N L S Q S T Q T I E A F S	180
541 TCACAGTTAGCAAAGTTAGGTTCTACTATATCGCAGGCTAAAGGTTCTCTAAATAGGA	600
181 S Q L A K L G S T I S Q A K G F S N I G	200
601 AACAAAGTTGCAAAACTAAATTCTAAACAAATCTGGTTGGAAATAATTACTGGT	660
201 N K L Q N L N F S K T N L G L E I I T G	220
661 TTGCTATCAGGCATTCTGCAGGCTTGCTTAGCGGATAAAAATGCATCGACTGGCAA	720
221 L L S G I S A G F A L A D K N A S T G K	240
721 AAAGTTGCTGCAGGTTTGATTAAGCAATCAAGTTATTGTAATGTAACAAAGCAATT	780
241 K V A A G F E L S N Q V I G N V T K A I	260
781 TCTTCATATGTTTAGCACAACGTGTTGCTGGTCTATCAACTACTGGTGCTGTTGCT	840
261 S S Y V L A Q R V A A G L S T T G A V A	280
841 GCTTTAATTACTTCATCGATTATGTTGGCAATTAGTCCTTGGCATTTATGAATGCAGCA	900
281 A L I T S S I M L A I S P L A F M N A A	300
901 GATAAATTCAATCATGCTAATGCTTGTAGTGGTAAACAAATTCCGAAAATTGGC	960
301 D K F N H A N A L D E F A K Q F R K F G	320
961 TATGATGGGATCATTATTGGCTGAATATCAGCGTGGTGGTACTATTGAAGCTTCA	1020
321 Y D G D H L L A E Y Q R G V G T I E A S	340
1021 TTAACTACAATTAGTACGGCATTAGGTGCAGTTCTGCTGGTGTTCGCTGCTGTA	1080
341 L T T I S T A L G A V S A G V S A A A V	360
1081 GGATCTGCTGTTGGTGCACCGATTGCACTATTAGTTGCAGGTGTTACAGGATTGATCT	1140
361 G S A V G A P I A L L V A G V T G L I S	380
1141 GGAATTAGAAGCGTCTAACACAGGCAATGTTGAAAGTGTGCTAACCGTTACAAGGT	1200
381 G I L E A S K Q A M F E S V A N R L Q G	400

# FIG -3-2

## Appendix A update-July 1999, continued

Bases 1201-2400  
Amino acids 401-800

1201	AAAATTTAGAGTGGAAAAGCAAAATGGCGGTAGAACTATTTGATAAAGGCTATGAT	1260
401	K I L E W E K Q N G G Q N Y F D K G Y D	420
1261	TCTCGTTATGCTGCTTATTAGCTAATAACTAAAATTTGAGCTAAATAAGAG	1320
421	S R Y A A Y L A N N L K F L S E L N K E	440
1321	TTGGAAGCTGAACGTGTTATTGCAATACCCAACAAACGTTGGGATAATAATTGGTGAG	1380
441	L E A E R V I A I T Q Q R W D N N I G E	460
1381	TTAGCAGGTATTACCAAATTGGGTGAACGCATTAAGAGCGAAAAGCTTATGCAGATGCT	1440
461	L A G I T K L G E R I K S G K A Y A D A	480
1441	TTTGAAGATGGCAAGAAAGTTGAAGCTGGTCCAATATTACTTGGATGCTAAACTGGT	1500
481	F E D G K K V E A G S N I T L D A K T G	500
1501	ATCATAGACATTAGTAATTCAAATGGAAAAAACGCAAGCGTTGCATTCACCTGCCT	1560
501	I I D I S N S N G K K T Q A L H F T S P	520
1561	TTGTTAACAGCAGGAACGTAAATCACGTGAACGTTAACTAATGGTAAATACTCTTATATT	1620
521	L L T A G T E S R E R L T N G K Y S Y I	540
1621	AATAAGTTAAATTGGACGTGAAAAACTGGCAAGTTACAGATGGAGAGGCTAGTTCT	1680
541	N K L K F G R V K N W Q V T D G E A S S	560
1681	AAATTAGATTCTCTAAAGTTATTCAACGTGAGCCGAGACAGAAGGCACAGACGAGATT	1740
561	K L D F S K V I Q R V A E T E G T D E I	580
1741	GGTCTAATAGTAAATGCAAAAGCTGGCAATGACGATATCTTGTGGTCAAGGTAAATG	1800
581	G L I V N A K A G N D D I F V G Q G K M	600
1801	AATATTGATGGTGGAGATGGACACGATCGTGTCTCTATAGTAAAGACGGAGGATTGGT	1860
601	N I D G G D G H D R V F Y S K D G G F G	620
1861	AATATTACTGTAGATGGTACGAGTGCAACAGAACAGCAGGTTATACAGTTAATCGTAAG	1920
621	N I T V D G T S A T E A G S Y T V N R K	640
1921	GTTGCTCGAGGTGATATCTACCATGAAGTTGTGAAGCGTCAAGAAACCAAGGTGGTAAA	1980
641	V A R G D I Y H E V V K R Q E T K V G K	660
1981	CGTACTGAAACTATCCAGTATCGTATTGAATTAAAGAAAAGTTGGTATGGTATCAG	2040
661	R T E T I Q Y R D Y E L R K V G Y G Y Q	680
2041	TCTACCGATAATTGAAATCAGTAGAGAAGTAATTGGTCTCAATTAAATGATGTATT	2100
681	S T D N L K S V E E V I G S Q F N D V F	700
2101	AAAGGTTCTAAATTCAACGACATATTCCATAGTGGTGAAGGTGATGATTACTCGATGGT	2160
701	K G S K F N D I F H S G E G D D L L D G	720
2161	GGTGTGGTGACGACCGCTTGTGGTAAAGGCAACGATCGACTTCTGGAGATGAA	2220
721	G A G D D R L F G G K G N D R L S G D E	740
2221	GGCGATGATTACTCGATGGCGTTCTGGTATGATGTATTAAATGGTGGTCTGGTAAT	2280
741	G D D L L D G G S G D D V L N G G A G N	760
2281	GATGTCTATATCTTCGAAAGGTGATGGAATGATACTTGTACGATGGCACGGCAAT	2340
761	D V Y I F R K G D G N D T L Y D G T G N	780
2341	GATAAATTAGCATTTGCAAGATGCAAATATATCTGATATTATGATTGAACTACCAAAGAG	2400
781	D K L A F A D A N I S D I M I E R T K E	800

# FIG 3-3

## Appendix A update-July 1999, continued

Bases 2401-2784

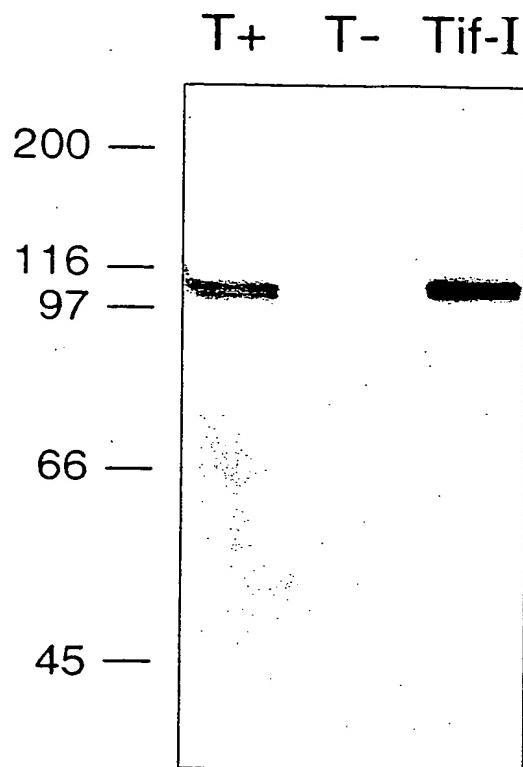
Amino acids 801-927

2401	GGTATTATAGTTAACGAAATGATCATTCAAGTAGTATTAACATACCAAGATGGTACATA	2460
801	G I I V K R N D H S G S I N I P R W Y I	820
2461	ACATCAAATTACAAAATTATCAAAGTAATAAAACAGATCATAAAATTGAGCAACTAATT	2520
821	T S N L Q N Y Q S N K T D H K I E Q L I	840
2521	GGTAAAGATGGTAGTTATATCACTTCCGATCAAATTGATAAAATTGGCAAGATAAGAAA	2580
841	G K D G S Y I T S D Q I D K I L Q D K K	860
2581	GATGGTACAGTAATTACATCTAAGAATTGAAAAAGCTTGCTGATGAGAATAAGAGCAA	2640
861	D G T V I T S Q E L K K L A D E N K S Q	880
2641	AAATTATCTGCTTCGGACATTGCAAGTAGCTTAAATAAGCTAGTTGGGTCAATGGCACTA	2700
881	K L S A S D I A S S L N K L V G S M A L	900
2701	TTTGGTACAGCAAATAGTGTGAGTTCAACGCCCTACAGCCAATTACACAACCAACTCAA	2760
901	F G T A N S V S S N A L Q P I T Q P T Q	920
2761	GGAATTTGGCTCCAAGTGTAG	SEQ ID NO: 1
921	G I L A P S V *	SEQ ID NO: 2

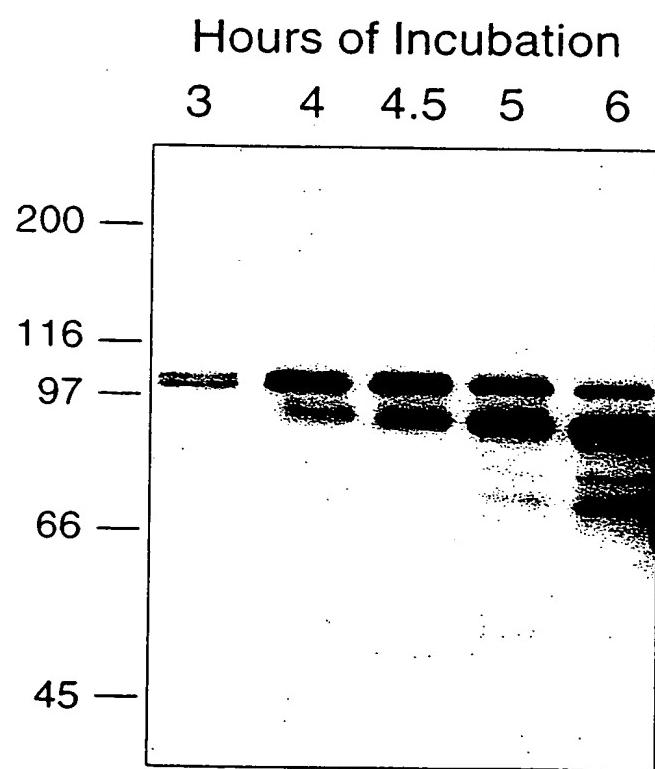
# FIG. 4

MdxA	- - - T R E I T T L S	N G L K N T L T A T	- - - M S N I N	V I K S N I Q A G L	N S T K S G L E N L	Y D A I P K . D K	D P O K G	38
LktA	- H G T R E I T T L S	N G L K N T L T A T	K S C L H K A G .	S S L K T S G A K K .	I L X X I P Q N Y Q M	. D S G Q G	59	
ApxIIA	H S K I T E S S L K	S S L Q Q G L E C	K H K L N Q A G T .	L K N Q L T Q T G .	I L X X I P O G . Q M	. D S G Q G	62	
HlyA	H P T I T A A Q L K	S T L Q S A K Q S A	A R K L H S A G Q S	T K D A L K K R A E .	Q T R N A G . N L L	I L M I P K D V K .	. D Q C	61
MdxA	G T L N D F Y K R A	D E L G I A R L A F	E P N H G E T A K K	S V D F V N Q F L S	L T T R G I A I S A	T K L E K F L O K H	S T N K L	103
LktA	G S G L O D L V K A R A	D E L G I B V O R E	E R N H G E T A K K	S L C C T I Q T A I G C	L T T R G I A I S A	P Q D K L L O K .	. T P K A	121
ApxIIA	H G V O D L V K A R A	N - L G I S B V U R E	E R N H G E T A K K	S F D C T I Q T A I G C	F T T R G I A I S A	P Q G D N L L K K .	. N P K A	125
HlyA	S S L N D L V . T A	D E L G I E V O T E	E R N H G E T A I T E Q	V F G C A K K L I C	L T T R G I A I S A	P Q G D K L L E Q K .	Q . K A	124
MdxA	A K G L . D S V E N	I D R K L G K R A S N	V L S T T S S F V C	T A L A C I E F L D S	L I K K . . . . G D	A A P D A L A K A S	I M I I N	163
LktA	G O A L L . G S A E S S	I S V Q N A N K A K T	V L S T T S S F V C	S V L A G Q M D L D S	A L O N . . . . G D	S N O H A L A K A S	I M I I N	180
ApxIIA	G S A S S S	I S O N E G R A N T	V L C G I O S S I E G C	S V L S S G V N L N E	L L Q N . . . . G D	P N O L E L A R A G S	I M I I N	185
HlyA	G N K E L G G S A S S	I G D N L G K A G S	V L S T T F O N F L G	T A L S S M K I D E	L I K K Q K S G G N	V S S S E L A R A S	I M I I N	189
MdxA	E W I G N W S Q S T	O T E W A F S S O L	A K L G S T T S Q A	K G F S N G N K L	O N L . N F S K T N	L G L D I I T G L L	S G I S A	227
LktA	S L I E B I A N S V	K T L D E P G R Q O I	S Q F G S K L Q N I V	K G L G T L G D R L	O N L . C G L D K A G	L G L D I I S G L L	S G A S A	245
ApxIIA	E L V V D T A A S V L	O T V D A F A E Q I	N K L G S H L Q N I V	K H L G G L S N K R L	Q N L E P D L G K A S	L G L D I I S G L L	S G A S A	250
HlyA	N N V N S P S . O L	N K L G S V L E S N T	K H L M O V G N R L	Q N L P N L D N I G	A G L D T U S G A L	S A I S A	253	
MdxA	G P A L A D K N A S	R G K K V A D A C	R E L S N Q V I G H V T	K A I S S Y T I L A Q	R V A A G L S T T G	A V A A L I T S S T	M L A R I S	292
LktA	G P A L A D K N A S	T A K K V G A D A C	R E L S N Q V I G H V T	R V R A A G L S T T G	R V R A A G L S T T G	P V A A L I A S T V	S L A R I S	310
ApxIIA	G L I L A D K E R S	T E K K A R A V C	R E L S N Q V I G H V T	R V R A A G L S T T G	R V R A A G L S T T G	P V A A L I A S T V	A L A R I S	315
HlyA	S F I L S N A D A D	T G T K A R A V C	R E L S N Q V I G H V T	R I C K I S Q I M A Q	R A A Q G L S T S A	A A A C L I A S V V	T L A R I S	318
MdxA	P L A F . N A A D K	F N H A N A L E E	A K O P K F G Y D	G D H L L A E Y O R	C V O G T I R A S L T	T I C K R L G R V S	A C V S A	357
LktA	P L A F G A I A D K	F N H A K S L E S X	A E R F K K L G Y D	G D H M L L A E Y O R	G T G T I D A S V U	A I N T A L R A I A	A C V S A	375
ApxIIA	P L S P L N . I A D K	P K Q A D L I K E P	S E R P F K K L G Y D	G D H M L L A E Y O R	G T G T I D A S V U	A I N T A L R A I A	A C V S A	380
HlyA	P L S F L S I A D K	P K R A N K I E P Y	S . S R P F K K L G Y D	G D S L L A A F H I	E T G T I D A S V U	R I C K C V L A S V S	S G M S A	383
MdxA	A A V G S A V C A P	I A L L V A G V T G	L I S C G I L E A S K	Q A M P E S V A N E	L O C K I K I L E W E K	Q N G C O N Y F E K	G Y D S R	422
LktA	A A C S V . A S P	I A L L V S Q S T G	V I S T I L E Y S K	Q A M P E P H V A N K	I H N H K I V E W E K	N N H G K N X P E K	G Y D S R	440
ApxIIA	A S A G S L V C A P	V A L L V A G V T G	L I T T I L E Y S K	Q A M P E P H V A N K	V H D H I V E W E K	-. K H G K N X P E O	G Y D S R	444
HlyA	A A T T S L V C A P	V S A L V G A V T G	L I T S C G I L E A S K	Q A M P E P H V A N K	M A D V I A E W E K	-. K R G K N X P E K	G Y D A R	447
peak 23								
MdxA	Y A R Y L A N N Z K	F L S C L N K E L Q	A E R V I A I T Q Q	R W D N N I G E L A	G I T L G E P I K	S C K A Y A D A F E	H G K V	487
LktA	Y L A N L O D E H M M K	F L I H I N K E L Q	A E R V I A I T Q Q	Q W D N N I G E L A	G I S R L Q E K . L	S C K A Z V D A F E	E G K H I	505
ApxIIA	H L R D L L O D E H M M K	F L I H I N K E L Q	A S G V V V A I T Q Q	H W D F D G D L A	A I S R E T D K Y S	S C K A Z V D A F E	E G Q H O	509
HlyA	H A B F L D D M F K	I L S Q Y N R E K Y S	V E R S V L I T Q Q	H W D F D G D L A	G W T R E N G D K T L	S C K S Y N D Y M E	E G K R L	512
MdxA	R A G . . . . S N T	T L D A K T G I I D	I S S N G N K K T Q	A L H F T S P L L T	A G T E S R E R L T	N C K Y G H I N K L	K F G R V	548
LktA	K A D . . . . K L V	Q L D S A N G I K I N	S E S S G K A K T Q	H M L P R T S P L L T	P G G E E N R E R R V O	T O G K R S V I T K L L	N H A Q R V	566
ApxIIA	S Y D . . . . S S V	Q L D N K N G I X I N	I S N T N R . K T Q	S V L P R T P L L T	P G G E E N R E R R V O	T O G K R S V I T K L L	N H A Q R V	569
HlyA	H K P K D E F Q K Q	V F D P L K G N I D	I S S D S . K S S T	L L K P V T P L L T	P G G E E N R E R R V O	S O K Y E P I T P E	L L K G V	575
MdxA	K N W Q V T D . C	A S S L D F S S K V	I Q R T A . . . . T	E G . . . . T D E I	G T I V N A K A G N	D D P F V Q G Q K M	N I D G C	605
LktA	D S W K V T D . G A	A S S E T F D L T S V	V V O R I G I E L O N D	A G N V T K T K E T	K I I A K L G E G D	D D N V F V G S G T T	V I D G G	610
ApxIIA	D S W K V T D . G A	D S W K V T D F T N V	V V O R I G I E L O N D	A G N I E S K T H	K I I A N L G A G N	D D N V F V G S S T T	V I D G G	613
HlyA	D S W T V K G V Q D	K G S V Y D J S N L	I O H A S V . . . .	A G N I E S K T H	K I I E S L G D D G	D K U F L S A G S A	N I Q Y A G	614
MdxA	D G H D R V F Y S C K	D G G C G N S T D	G R S A T E S A G S	T V N R K V U . A R C	D I Y H E V V K R Q	E T K V G K R T E T	I Q Y R D	669
LktA	D G H D R V F Y H Y S R	D G N K X C A L T I D	A T H E R E B Q G S	T V N R K V U . E T G	K A L B E V T S T A T H	T A L V G C N R E E E K	I Q Y R D	692
ApxIIA	D G H D R V H Y S R	D G Y C A L V I D	C T H A R E A G N Y	S U M R E G V G D S	K A L B E T T A T H	T A L V G C N R E E E K	I Q Y R D	695
HlyA	M G H D V V V Y D K	T . D T G Y L T I D	T V T R V L C G D V	K V L Q E V V K E Q	K V L Q E V V K E Q	E V S V G K R T E T	T O Y R S	698
peak 26								
MdxA	Y E L R K V . C Y G	X O S T D N L K S V	B E M I G S O F N D	W P K G S K F N D Y	F H S G M G D D L M	D D G C A G D D R L P	G G K G N	733
LktA	W S N N Q H . H A G G	X Y T K D T L K A V	E E I I G G T S H N D	I P K G C S K F N D A	F N C G D G C V D T I	D G N D G C N D R L P	G G K G N	756
ApxIIA	R E D D K R F . H T G	X Y T V T D S L R S V	E E I I G G S O F N D	K P F D D A	F H O G G N C V D T I	D G N D G C N D R L P	G G K G N	759
HlyA	Y E T H R I N G G N	L T E T D N L Y S V	E E I I G G T T R A D	K P F F G S K F A D I	F H G A D G D D H I	D G N D G C N D R L P	G G K G N	763
MdxA	D R L S G D E G D .	Y O L G G G D G N D K	L I G G A G G N N Y L	N G G D G D D E L Q	V Q G N S L A K N V	L S G G K G N D K L	Y G S E G	828
LktA	D D D G G G H G D .	Y O L G G G D G N D K	L I G G A G G N N Y L	N G G D G D D E L Q	V Q G N S L A K N V	L S G G K G N D K L	Y G S E G	828
ApxIIA	D D D G G G H G D .	Y O L G G G D G N D K	L I G G A G G N N Y L	N G G D G D D E L Q	V Q G N S L A K N V	L S G G K G N D K L	Y G S E G	828
HlyA	D D D G G G H G D .	Y O L G G G D G N D K	L I G G A G G N N Y L	N G G D G D D E L Q	V Q G N S L A K N V	L S G G K G N D K L	Y G S E G	828
MdxA	D L D G G S G G D .	D V S N G G A G N D O	N Y T F R K G D O N	D T T Y D G T G . N	D K L A F A D A N M	S D M I E R T K E	G G I M K	805
LktA	D D F D G G G H G D .	D L L H G G C K C D D	I V V H R K G D G D N	D T T Y D G T G . N	D K L L A F A D A N M	K D L T P E K V R H	N L A I	827
ApxIIA	N F L V G G G T G E	D L L H G G C K C D D	I V V H R K G D G D N	D S I T D S D C G . Q	D K L L S A F S D V A L	K D L T P E K K U D S	S L E I	830
HlyA	A D L D D G G G E G N	D L L K G G Y G G N D	I V V H R K G D G D N	H I I D D D G G C D	D K L L S A F S D V A L	K D L T P E K K U D S	D L I H Y	893
MdxA	R N D . . . . .	H S G S I N T P R W	W . . . . . I T S N L	O N Y Q S N K T D H	K I E O T I G K D G	S Y I T S D Q T P K	W L Q D K	859
LktA	T N S . . . . .	K K E K V T I T Q N H	P R E A D P L A S T V	P N X K E A T K . D R	K I E E K I G Q N G	S E R I T S K O V D D	L I I . K	882
ApxIIA	I N Q . . . . .	K G E K V T I R G N H	P F E D D O L A S T V	A N X K E A T K . D R	K I E E K I G Q N G	S E R I T S Q V D K	L I I . K	885
HlyA	K A E G N V L S I G	H K H G I T F K R W	P E K E . . . . S G D A I	S N . . . . Q	K I E O I F D K D C	R V I T P D S L K K	A L E Y Q	949
MdxA	H D G T V I T S C P	L K K L A D E N K S	O K L S A S D T A S	S L N K L M G C S M A	L P G T A N S V S S	N A L Q P I T Q P T	O C I I A	924
LktA	H G H G M I Q Q D Z	L S K V V D N Y E L T	L K L S K N V T S	S L D K L I S S V S	N A L Q P I T Q P T	N V L I . V . P T	O C I I A	941
ApxIIA	Z G H H O I S A G A	L S K V V D N Y E L T	S K . D R Q H V U S S	S L A K L I S S V G	S P . T S S S D F R	N N L Q T I V . P S	O S H E D	945
HlyA	Q S H R K . A S T V	Y G N D A L A Y G S	S Q G N L N P L Y N	E U S K A I S A A C	N P D V K E E R A A	A S L L Q L S G . N	A S D F S	1011
MdxA	P S V . . . . .	—	— 927					
LktA	Q S L S S M Q F A R	—	— 953					
ApxIIA	V S N N N I Q L A R	—	— 956					
HlyA	Y G R N S I T L T A	S A	1023					

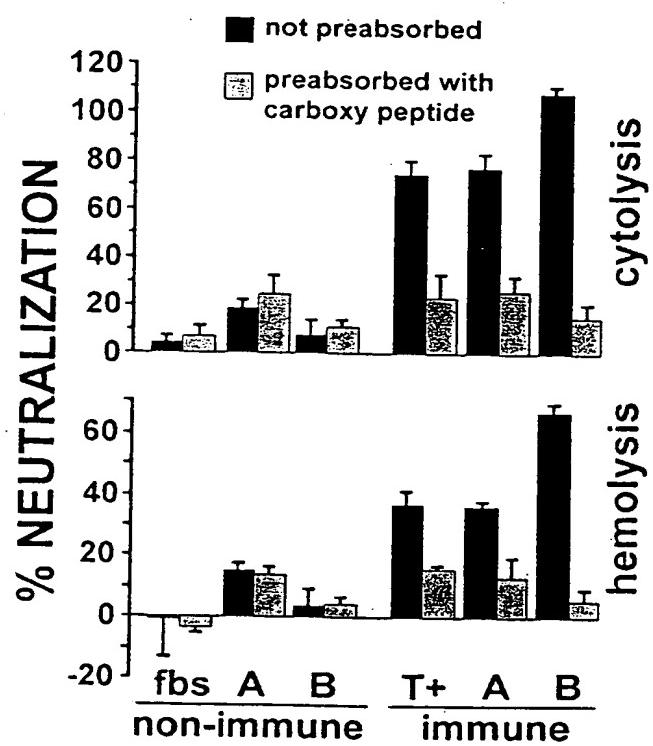
**FIG.5**



**FIG.6**



F16.7



UNASIS TRANSLATION EDITION LII-000 B genie.univ			
1 ATGGGTGGTGAATCTCTTAATTAGACTTAATTTACAAACCTTAATAGTAATTAGTT	60		
1 M G G D T S L I R N L Q T L N S N L V			
61 ATGATAGATTATGCTCAACAACCTGCTCATCTGCTCTGGTTATCCTGCCAAATACTAT	120		
21 M I D Y A Q Q P A L S A L V I L A K Y Y	40		
121 GGTATTTCTGCAAGTCAGCAGACATTATGCATCAGTTTCTGATAATACAAAAGGAGAC	180		
41 G I S A S P A D I M H Q F S D N T K G D	60		
181 CTGAATGAAATTGAATGGATGTTGGCAGCAAAGAAATTAGAATTAAGGTAAGATTATA	240		
61 L N E I E W M L A A K K L E L K V K I I	80		
241 AACAGCCTTAACCGATTGTCAATGATAACACTCCTGCTTGGTGTGGTGTGATAAT	300		
81 K Q P L T R L S M I T L P A L V W C D N	100		
301 AAGCCGATTAGATCAAAATTAAACTCTCATTTATACAACTAAATTGATGGGTG	360		
101 K P D L D Q N L N S H F I L T K I D G V	120		
361 GGATCTGCTGAAAATATCTCATCTACGATTGATTGAGAATCGTCCATAATATTAGAT	420		
121 G S A A K Y L I Y D L I E N R P I I L D	140		
421 GCAAGTGAGTTCTGAAAGATATTGTAAGTTATGCTAGTAACCTCCGTGCGTCA	480		
141 A S E F S E R Y S G K L M L V T S R A S	160		
481 ATATTGGTTCAATTGGCTAAATTGATTACTTGGTTATTCTGCGGTAAATCAAATAT	540		
161 I L G S L A K F D F T W F I P A V I K Y	180		
541 CGTTATATTGGTTGAAGTCATCGTTATTCACTGGTGTACAGATTGCTCTGATT	600		
181 R Y I F F E V I V I S V V L Q I F A L I	200		
601 ACGCCATTGTTTCAAGTTGTGATGGATAAGGTATTGGTCATCGTGGTTTCTACT	660		
201 T P L F F Q V V M D K V L V H R G F S T	220		
661 CTGGATGTGGTAGCGATTGCCCTGGTAGTAAGTTATTGAAGTCATTAAAGTGGT	720		
221 L D V V A I A L L V V S L F E V I L S G	240		
721 CTACGCACTTATATTGGCTCATACAAACCTCTGAATTGATGTAGAGCTAGGAGCACGA	780		
241 L R T Y I F A H T T S R I D V E L G A R	260		
781 TTATTTCGTCACTATTAGCTACCGCTTGGTTATTGAGAGTAGAAGAGTAGGCGAT	840		
261 L F R H L L A L P L A Y F E S R R V G D	280		
841 ACAGTTGCACTACGTGAATTGGAACATATCCGCAATTCTTAACGGTCAAGCTCTC	900		
281 T V A R I R E L E H I R N F L T G Q A L	300		
901 ACTTCAGTTAGATTGGTGTCTTATATTCTGTTGTAATGTGGTATTACAGC	960		
301 T S V L D L V F S F I F L F V M W Y Y S	320		
961 CCTACTAAACACTGGTAGTTGGCATCATTACCAATATGCGTTGGTCTGCC	1020		
321 P T L T L V V L A S L P I Y A F W S A F	340		
1021 ATTAGCCAATTACGCACCGACTAAATGATCAATTGCACTCGCAATGCGAGATAATCAA	1080		
341 I S P I L R T R L N D Q F A R N A D N Q	360		
1081 TCTTTTTAGTGGAAAGTATTACTGCGGTTGGTAGCGTAAAGCAATGGCAGTTGAACCT	1140		
361 S F L V E S I T A V G T V K A M A V E P	380		
1141 CAAATGACCGTCGGGATAATCAATTAGCAGCTTATGTGGTTCTAGTTGGTA	1200		
381 Q M T R R W D N Q L A A Y V V S S F R V	400		
1201 GCTAAGTTGGCAATGGTGGCAGCAAGGAGTACAACCTATTCAAAAGATGGTTATTGTG	1260		
401 A K L A M V G Q Q G V Q L I Q K M V I V	420		
1261 GCAACTCTATGGATTGGTCAAAATTGTAATTGAAGGCAAGCTATGGTAGGTCAATT	1320		
421 A T L W I G A K L V I E G K L S V G Q L	440		

8-1  
misx b  
p/bx

DNA sequence		Start Position	End Position
1321	ATAGCATTTAATATGCTGGCAGGTCAAGTGGCCGCTCTGTTATCGCCTGGCACAGCTA		1380
441	I A F N M L A G Q A A P V I R L A Q L		
1381	TGGCAAGATTTCAAGCAAGTAGGTATTCACTGGCAGATTGGGTGATATTTAAACT		1440
461	W Q D F Q Q V G I S V A R L G D I L N T		480
1441	CCAAC TGAGCATTCTACATCTCGCTTAACCTTACCTGATATTAAGGGTGATATTACATT		1500
481	P T E H S T S R L T L P D I K G D I T F		500
1501	GAAAATGTTGATTTTCGCTACAAAATAGATGGGCATTAAATATTACAGAATTAAATT		1560
501	E N V D F R Y K I D G H L I L Q N L N L		520
1561	CAGATTAACGCTGGAGAGATACTAGGTATCGTAGGACGCTCTGGTTCAAGTAAATCAACA		1620
521	Q I N A G E I L G I V G R S G S G K S T		540
1621	TTGACAAAATTAGTACAGCGTTATATGTACCGAGAAAATGGCGAATATTAGTTGATGGA		1680
541	L T K L V Q R L Y V P E N G R I L V D G		560
1681	AACGATTGCGATTAGCTGATCCCGCTGGCTGCGTCGCCAAGTGGGTGTTGTTGCAG		1740
561	N D L A L A D P A W L R R Q V G V V L Q		580
1741	GAAAATGTGTTACTCAATCGTAGTATTGAGATAATATTGCCCTAACGTACACGGGATG		1800
581	E N V L L N R S I R D N I A L T D T G M		600
1801	TCATTAGAGTTTATTATCCAGGCTGCCAAGATGTCGGGGCACATGACTTTATTATGGAA		1860
601	S L E F I I Q A A K M S G A H D F I M E		620
1861	TTGCCCTGAGGGTTATGATACGATTGTTGGAGAGCAAGGTGCAGGCTTGTCAAGGTGGACAA		1920
621	L P E G Y D T I V G E Q G A G L S G G Q		640
1921	CGCCAGCGTATCGTATTGCGCGTCTTAATTACCAATCCGCTATTTGATTTTGAT		1980
641	R Q R I A I A R A L I T N P R I L I F D		660
1981	GAAGCTACTAGTCGATTAGACTATGAGTCGAAAGGGCTATTATGCAAAATATGCAGGCA		2040
661	E A T S A L D Y E S E R A I M Q N M Q A		680
2041	ATTTGCCAAGGTAGAACAGTGTGATTATTGACATCGCTTATCTACCGTAAAAATGGCA		2100
681	I C Q G R T V L I I A H R L S T V K M A		700
2101	CATCGCATTATTGCAATGGACAAGGGAAAATTGTAGAGCAAGGCACACATCAAGAATTG		2160
701	H R I I A M D K G K I V E Q G T H Q E L		720
2161	TTGCAAAAGAAGATGGTTACTATCGTTATATGATTGAGAATGGATAAA		2215
721	L Q K E D G Y Y R Y L Y D L Q N G *		739

F16.8-2

# F16.9

MbxB	-----MID	Y A Q Q P A L S A	L V I L A K Y I C	I S A S P A I H	H Q F S D N T K G	D L N E I E W M L	A A K K L B L	55
LktB	M A N B O R N D	L . . . . . G L V A	L T M I A Q Y H N	I S L E P E E I K	H K P D L D G R G	D L S L T A W L L	A A K S L A L	56
ApxIB	K D F Y R E . E D	Y . . . . . G L Y A	L T I L A Q Y H N	I A V E P E E I K	H K P D L G R G	D L D L T A W L L	A A K S L E E	55
HlyB	M D S C H K . I D	Y . . . . . G L Y A	L E I L A Q Y H N	S V E P E E I K	H F D T D G T G	D L G L T S W L L	A A K S L B I	55
MbxB	R U X I I K Q P T	T H E S M I T T L P	A L V W C D N K P	D L D Q N L N S H	P I L T K I D G V	G S R A K Y L I Y	D L I T N R P	116
LktB	N A R H I K K E I	S R L H L N L P	A L V W Q D N . . .	A L V W R E D . . .	P I L T K I D . . .	T N H R Y I L T Y	N L E Q D A E	107
ApxIB	K A K Q V K K A X	D R L A P I A L P	A L V W R E D . . .	.. . . . . G K H	P I L T K I D . . .	N E A K K Y L I F	D L E T H N F	106
HlyB	K V Q V K R K T I	D R L N P I S L P	A L V W R E D . . .	.. . . . . G K H	P I L T R V S . . .	K E A N R Y L I F	D L E Q R N F	106
MbxB	I I L M A S E P S	E R Y S G K L H M L	V T S R A S I L G	S L A K P D F T W	P I P A V I K Y R	Y I P F E V V V	S V V L Q I F	177
LktB	Q I L S T D R E P E	A C V Q G Q G L L	V T S R A S I V V G	S L A K P D F T W	P I P A V I K Y R	R I P I E T L I V V	S I P L Q I F	168
ApxIB	R I L E Q A E P E	S L Y Q G K L L I L	V A S R A S I V G	S L A K P D F T W	P I P A V I K Y R	R I P I E T L I V V	S I P L Q I F	167
HlyB	R I L E Q S E P E	A L Y Q G H . I L	V A S R S B V A G	S L A K P D F T W	P I P A V I K Y R	R I P I E T L I V V	S V P L Q I F	167
MbxB	A L I T P L F F Q	V V M D K V L V B	R G F S T L D V	A . A L L V V S L	P E I I L S G L R	T Y I F A H T S	R I D V E L G	238
LktB	A L I T P L F F Q	V V M D K V L V B	R G F S T L N I	T V A L A I V . . .	P E I I L S G L R	T Y P S R S T S	R I D V E L G	229
ApxIB	A L I T P L F F Q	V V M D K V L V B	R G F S T L H V I	T V A L A I V V . .	P E I I L S G L R	T Y I F A H S T S	R I D V E L G	228
HlyB	A L I T P L F F Q	V V M D K V L V B	R G F S T L N V I	T V A L S V V V V	P E I I L S G L R	T Y I F A H S T S	R I D V E L G	228
MbxB	A R L P R H L L A	L P M A X P E S R	R V G D T V A R . .	R E L D M I R H F	L T G Q A L T S V	L D L V F S P I F	L F V M W X Y	299
LktB	A K L P R H L L S	L P I S Y P E N R	R V G D T V A R V	R E L D Q I R H F	L T G Q A L T S V	L D L L F S P I F	F A V M W X Y	290
ApxIB	A R L P R H L L A	L P I S Y P E N R	R V G D T V A R V	R E L D Q I R H F	L T G Q A L T S V	L D L L F S P I F	F A V M W X Y	289
HlyB	A K L P R H L L A	L P I S Y P E S R	R V G D T V A R V	R E L D Q I R H F	L T G Q A L T S V	L D L L F S P I F	F A V M W X Y	289
MbxB	S P A L T L V L	A S L P I Y A F W	S A F I S P I L R	T R L N D O F A R	H A D N Q S P L V	E S T A T G T	K A M A V E P	360
LktB	S P K L T L V I L	G S L P C Z I L W	S I F I S P I L R	T R L N D E K F A R	H A D N Q S P L V	E S V T A I N M I	K A M A V A P	351
ApxIB	S P K L T L V I L	G S L P F Y M G W	S I F I S P I L R	T R L N D E K F A R	G A D S Q S P L V	E S V T A I N M I	K A M A V T P	350
HlyB	S P K L T L V I L	F S L P C Y A W W	S I F I S P I L R	T R L N D D K F S R	N A D N Q S P L V	E S V T A I N T I	K A M A V S P	350
MbxB	Q M T F R H D D Q	L A A Y V V S S F	R V A K L R M C	Q Q C V Q L I Q K	M V I V A T E W N	G A K L V I E G K	L S G Q L I	421
LktB	Q M T D T W D B Q	L A S Y V V G S S P	R V T V L A T I G	Q Q C V Q L I Q K	T V V M V I N L W L	G A H L V I S G D	L S I G Q L I	412
ApxIB	Q M T H T W D B Q	L A S Y V V S A G F	R V T T L A T I G	Q Q C V Q F I Q K	T V V M V I T E W L	G A H L V I S G D	L S I G Q L I	411
HlyB	Q M T H T W D B Q	L A G T V A A G F	R V T V L A T I G	Q Q G Q L I Q K	T V M I N I L W L	G A H L V I S G D	L S I G Q L I	411
MbxB	A P H M L A G Q V	A A P V I R L A Q	L W Q D F Q Q V G	I S V A R L G D M	L N T P T E H S T	S E I T L P I K	G D I T P E N	482
LktB	A P H M L S G Q V	I A P V I R L A Q	L W Q D F Q Q V G	I S V T R L G D V	L E S P T E Q X Q	G R L A L P E I K	G D I S P H	473
ApxIB	A P H M L S G Q V	I A P V I R L A Q	L W Q D F Q Q V G	I S V T R L G D V	L H S P T B S T Q	G R L A L P E I K	G D I T P R N	472
HlyB	A P H M L A G Q V	I A P V I R L A Q	L W Q D F Q Q V G	I S V T R L G D V	L H S P T B S Y H	G R L A L P E I K	G D I T F R E	472
MbxB	W D P R Y K I D G	H L I L Q P L N L	O I N A G B E F G	I V G R S G S G K	S T L T K L I Q R	L Y P E N G R T	L D G N D L	543
LktB	I R P R Y K P D A	P T I L B H V U S L	E I R Q Q G E V I G	I V G R S G S G K	S T L T K L I Q R	F X I P E N G Q V	L I D G H D L	534
ApxIB	I R P R Y K P D A	P F V I L H D V E L	S I Q Q G E V I G	I V G R S G S G K	S T L T K L I Q R	F X I P E N G Q V	L I D G H D L	533
HlyB	I R P R Y K P D S	P V I L D N E N L	S I K Q G E V I G	I V G R S G S G K	S T L T K L I Q R	F X I P E N G Q V	L I D G H D L	533
MbxB	A L A D P A N L R	R Q V G V V L Q	H V L L N R S I R	D E I A L T D G	M S F E F I I Q R	A K L A G A H D F	I M B I P E G	604
LktB	A L A D P H W L R	R Q G V V V L Q D	H V L L N R S I R	D E I A L T D G	M P F H E V V Y A	A K L A G A H D F	I S E L R E G	595
ApxIB	A L A D P H W L R	R Q V G V V L Q D	H V L L N R S I R	D E I A L T D G	M P M E K I . . . A	A K L A G A H D F	I S E L R E G	594
HlyB	A L A D P H W L R	R Q V G V V L Q D	H V L L N R S I T	D W I S L A N P C	M S V E R V I T A	A K L A G A H D F	I S E L R E G	594
MbxB	X D T I V G E Q G	A G L S C G Q R Q	E I A I A R A L M	T N P I X I L I P D	E A T S A L D Y E	S E R A I M Q R M	Q A I C O G R	665
LktB	X I T I V G E Q Q	A G L S C G Q R Q	E I A I A R A L V	T N P I X I L I P D	E A T S A L D Y E	S E H I I M Q R M	Q K I C O G R	656
ApxIB	X I T I V G E Q Q	A G L S C G Q R Q	E I A I A R A L V	T N P I X I L I P D	E A T S A L D Y E	S E H I I M R E M	H Q I C K G R	655
HlyB	X I T I V G E Q Q	A G L S C G Q R Q	E I A I A R A L V	T N P I X I L I P D	E A T S A L D Y E	S E H I I M R M	H K I C K G R	655
MbxB	T V I I X A H R L	S T V K H A D R I	I A M E G K I V	E Q C H Q E L L	Q K E D G Y Y R Y	L Y D L Q N G	717	SEG ID NC 18
LktB	T V I I X A H R L	S T V K H A D R I	I V M E K G E I V	E Q C K H H E L L	Q N S H G L Y S Y	L H Q L Q L N	708	SEG ID NC 19
ApxIB	T V I I X A H R L	S T V K H A D R I	I V M E K G Q I V	E Q C K H K E L L	A D P H Q L Y H I	L H Q L Q S E	707	SEG ID NC 20
HlyB	T V I I X A H R L	S T V K H A D R I	I V M E K G I V	E Q C K H K E L L	S E P E S L Y S Y	L Y Q L Q S D	707	SEG ID NC 21

# FIG. 10

DNASIS Translation Editor [11-00 C gene.dna]

1 ATGACGAAAAAGTTGCAGAGCTAGGTTAATTGCATGGCTTGGCTAACCTGTATG	60
1 M T K K F A E L G L I A W L W S N S D M	20
61 CATAAACATTGGACGTTGTCTTGTGCGACCAATGTTATTCCGGCAATTGAGACAGGT	120
21 H K H W T L S L F A T N V I P A I E T G	40
121 CAATATGTTATATTGAAAAGAGAAGATATGCCGTAGCATATTGAGTTGGCTAAACTT	180
41 Q Y V I L K R E D M P V A Y C S W A K L	60
181 AGTTTAGAAAAGAGGTTAAATATATTAAACGATGTTACTTCTCTTAAGTTAGATGACTGG	240
61 S L E N E V K Y I N D V T S L K L D D W	80
241 CAGTCAGGTGACCGAAACTGGTTATTGACTGGATTGCTCCATTGGCGATAGTCTTACA	300
81 Q S G D R N W F I D W I A P F G D S L T	100
301 CTCACAAAACACATGAGAACGTTATTTAGATGAATTGTTAGAGCGATTGTAGAT	360
101 L T K H M R T L F S D E L F R A I R V D	120
361 GGAAATTCAATCGATGTAAGATATCTGAATTGGAAAGTCTGTTGATTCAAATTA	420
121 G N S S H G K I S E F Y G K S V D S K L	140
421 GCCTCAAGAATATTGACAATATCACGAAGATTGACGAGCAAATTGTCAACTCAGAAT	480
141 A S R I F A Q Y H E D L T S K L S T Q N	160
481 AATTTTATTATATCTAAAGATAATTAA	507
161 N F I I S K D N *	169

m<sup>b+</sup> C  
 m<sup>b+</sup> C  
 M<sup>b+</sup>

# FIG. 11

MbxC	---	M T K K F A E	L G L I A W L W S N	S D H K H W T L S	L F A T N V I P A I	E T G Q Y	42
LktC	--	M N Q S Y F N L	L G N I T W L W M N	S S L H K E W S C E	L L A R H V I P A I	E N E Q Y	43
ApxIC	M S K K I N G E F E V	L G E V A W L W A S	S P L E R K W P L S	L L A I N V L P A I	E S N Q Y	45	
HlyC	- M N R N N P L E V	L G H V S W L W A S	S P L H R N W P V S	L F A I N V L P A I	R A N Q Y	44	

MbxC	V L K R D M P V	A Y C S W A K L S L	E N E V K Y I N D V	T S L K L D D W Q S	G D R N W	87
LktC	M L L I D N G I P I	A Y C S W A D L N L	E T E V R V Y I K D V	N S L T P E R W Q S	G D R R W	88
ApxIC	V U L L K R D G F P I	A M C S W A N L N L	E N E I K Y L D D V	A S L V A D D W T S	G D R R W	90
HlyC	A L L T R D N I P V	A Y C S W A N L S L	E N E I K Y L N D V	T S L V A E D W T S	G D R M W	89

MbxC	F I D W I A P F G D	S L T L T K H M R T	L F S D E L F R A I	R V D G N S S . H G	K I S E F	131
LktC	I I D W I A P F G H	S Q L L Y K X M C Q	R K P D M V R S I	R F Y P R Q K E L G	K I A Y F	133
ApxIC	F I D W I A P F G D	S A A L Y K H M R D	N F P N E L F R A I	R V D P D S R . V G	R I S E F	134
HlyC	F I V W I A P F G D	N G A L Y K E M R K	K F P D E L F R A I	R V D P R T H . V G	R N S E F	133

MbxC	S G K S W D S K L A	S E I F A Q Y H E E M	L T S K L S T Q N N	F I I S K D N -	168
LktC	K G G K D D K E T A	K K R F D T Y Q E E	L A T A L K N E F N	F I K K - - -	167
ApxIC	H G G K I D K K L A	S K I F O Q Y H F E	L M S E L K N K Q N	F K F S L V N S	172
HlyC	H G G K I D K Q L A	N K I P K O Y H H E	L I T E V K N K S D	P N F S L T G -	170

SEQ ID NO: 32  
 SEQ ID NO: 33  
 SEQ ID NO: 34  
 SEQ ID NO: 35

## DNASIS translation editor [11-00 v gene.aaa]

60 F1612-1

1 ATGTTTATACAAGCACTAAAGATT	TTTATTTCGCTATATAACC	GTTGGCGCAATACA	60
1 M F I Q A L K D F	I R Y I T V W R N T		
61 TGGGCAGTTCGAGACCAACTAACCCCTCCTAAGCGTACTAAAGAAGAACTCGCTTCTT		120	
21 W A V R D Q L T P P K R T K E E L A F L		40	
121 CCTGCACATCTAGAACTCACTGACACACCTGTATCCAGATCTTAAGTGGACAGCTAGA		180	
41 P A H L E L T D T P V S R S S K W T A R		60	
181 ATAATCATGATATTGCTTATTGCTATGGTCTGGGTTGGACAGATTGACATT		240	
61 I I M I F V L F A L L W S W V G Q I D I		80	
241 GTTGCTACAGCTTCAGGTAAGATTCTTCAGGTAGCCGTAGCAAGACTATTCAATCTTG		300	
81 V A T A S G K I S S G S R S K T I Q S L		100	
301 GAAACAGCGATAGTTAAAGCAGTTATGTACGTGATGGTCAAATGTTCAACAAGGTGAA		360	
101 E T A I V K A V Y V R D G Q N V Q Q G E		120	
361 ATATTAGTAGATTAGTGGGAATCGGTTCAAGATAGTGTAGTCTAGTCAGTCCGAGAAAGCC		420	
121 I L V D L V G I G S D S D V A Q S E K A		140	
421 CTTCGAGCGCGCAATTATCTAACGCTACGCCCTGAAGCAATTATCAGCATTAAATCAC		480	
141 L R A A Q L S K L R L E A I L S A L N H		160	
481 CGTATTAACTCTCAGATTGATGTAGCATATGCAAAGTCTTAAATATTTCAGAACATCGGAA		540	
161 R I N P Q I D V A Y A K S L N I S E S E		180	
541 ATTAATGAAGCTCAAACCTTACGCCAAATCAATATCAAGCATGGTTAGCACAAGATGAA		600	
181 I N E A Q T L A Q N Q Y Q A W L A Q D E		200	
601 CAACTAAAATTAAACCTTAAAGGACATCAAGCAGAATTACAATCTGCTCGATCCCAAGAA		660	
201 Q L K L T L K G H Q A E L Q S A R S Q E		220	
661 CAAAAGTTGGTTCAAGTGGCAATTGAACATCAAAGACTGATGATTATCGGAGTCTC		720	
221 Q K L V S V G A I E H Q K T D D Y R S L		240	
721 AAAGCAGAAAATTATATCTGAGCATGCTTATCTAGAACAGAAAGCAAATTACTTAGC		780	
241 K A E N F I S E H A Y L E Q E S K L L S		260	
781 AATCAAAATGATTACAAAGTACACGTAGTCAGATTCAAAAAACAGGCTGCAATCATG		840	
261 N Q N D L Q S T R S Q I Q K I Q A A I M		280	
841 CAAGCTGAACAGAACCGTATGTTATATACTCAAAATCTAAACGTGATACTAGAACATCT		900	
281 Q A E Q N R M L Y T Q N L K R D T L E S		300	
901 TTACGCCAACCAATGAACAGATTAATCAATATACTGGTCAAACATAAAAGCTAACAGCAG		960	
301 L R Q T N E Q I N Q Y T G Q T N K A K Q		320	
961 CGACAGAAATTGCTGAGTATTAAATCACCTGTTAATGGTACTATACAAGAGCTAACAGCT		1020	
321 R Q K L L S I K S P V N G T I Q E L T A		340	
1021 TATACTTTAGGTGGAGTTGACAAGCAGCACAAAAATTATGGTGTGGCACCTAACGAT		1080	
341 Y T L G G V V Q A A Q K I M V V A P N D		360	
1081 AATCAAGTGGAAAGTAGAGGTATTAGTGTAAATAAGATATCGGCTTGTAAAAGCTGGG		1140	
361 N Q V E V E V L V L N K D I G F V K A G		380	
1141 CAGAATGTTATCATCAAATCGAGAGTTCTTATACACGTTATGGTTATTAACAGGT		1200	
381 Q N V I I K I E S F P Y T R Y G Y L T G		400	
1201 AAAATAAAAAGTATTAGTCATGATGCTATAGAACATCAACATTAGGTCTAGTGTACT		1260	
401 K I K S I S H D A I E H Q H L G L V Y T		420	
1261 GCACTTGTCTCTGATAAAAGCACATTAATAGATGGAGTAACAATCAACTAACG		1320	
421 A L V S L D K S T L N I D G V T I N L T		440	

UNASIS translucens cultv. L-1700 v. geniculata  
1321 CCAGGAATGAATGTTACTGCTGAAATTAAAACAGGTAAACGTCGTGTTGGATTATATA 1380  
441 P G M N V T A E I T G K R R V L D Y I  
1381 TTAAGTCCATTGCAGACAAAAGTTGATGAAAGTTTCGAGAACGCTAA 1428  
461 L S P L Q T K V D E S F R E R \* 476

FIG. 12-2

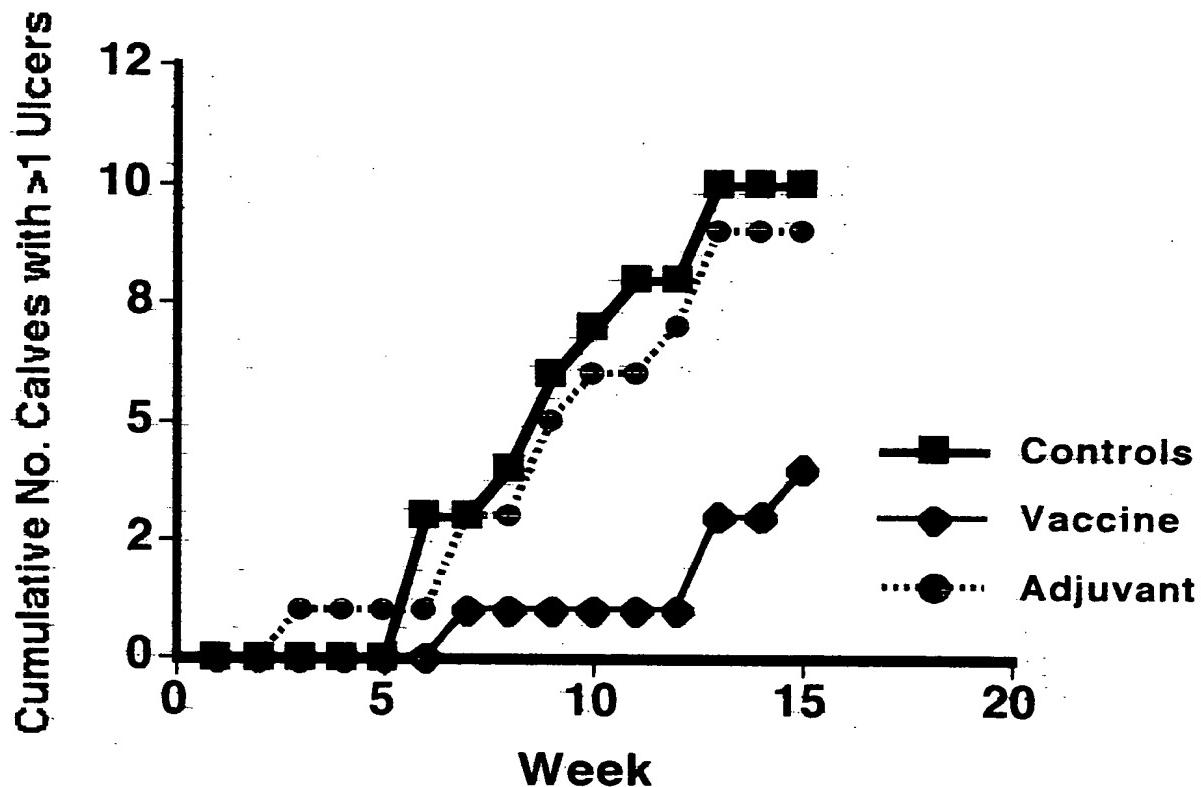
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**FIG. 13**

MbxD	- - M F Q Q A L K	F F R Y I T V W R	N T W A F R D Q L T	P P K R T K E L A	F L P A H E L I E	48
LktD	M K I W L S G Y E	F F L R Y K N W A	E V W K I R K Q L D	H P N R K R D E S E	F L P A H E L I E	50
ApxID	M K T W L M G L Y E	F F Q R Y K T V W T	E I W K I R H Q L D	T P D R E K D E N E	F L P A H E L I E	50
HlyD	M K T W L M G F S E	F L L R Y R L V W S	E T W K I R K Q L D	T P V R E K D E N E	F L P A H E L I E	50
MbxD	T P V S R S S W T	A R I I M F V L F	A L L W S W V G Q	E I V A T A S G K	S S G S R S K T I Q	98
LktD	T P V S K K P R L I	A Y L I M L F L V V	A V L A S V S K V	E I V A T A P G K L	T F S G R S K E I K	100
ApxID	T P V S K K P R L I	A Y L I M L F L F L	A L V S I V S H V	E I V A T A T G K L	A F S D R S K E I K	100
HlyD	T P V S R P R L I	A Y F I M G P L V I	A F L S V L G Q V	E I V A T A N G K L	T I S G R S K E I K	100
MbxD	S I E T A I V K A	F V M D G Q N V Q	G E L V D L V G	G S D S D V A Q S E	K A L R A R Q L S K	148
LktD	P I E N A I V Q E I	F V K D G Q F V E K	G Q L L V S L T A L	G S D A D I K K T M	A S L S L A K L E N	150
ApxID	P I E N A V K E I	F V Q D G Q F V E K	D Q L L L H L T A L	G A D A D Q K T K	S S L S L T K L E R	150
HlyD	P I E N S I V K E I	I V K A G E S V R K	G D V U L L K L T A L	G A A D T L K T Q	S S L L Q R A L E Q	150
MbxD	L R L E A I L S A	N R R I N P Q I D V	A Y A K S L N I S	E S E I N E A Q T L	A Q N Q Y Q A W L A	197
LktD	Y R Y Q T I L L T A Y	E K E S L P V I D L	. S R T E F K D S S	E E D R L R I K H L	I E E Q Y T T W Q R	199
ApxID	Y R Y E T I L L E A	A A D R L P L I L I	. T K D E F R K A T	E E D K T R I Y R L	I T E Q F E A W Q R	199
HlyD	I R Y Q I I L S R S I	E L N K L P E E K L	P D E P Y F Q N V S	E E E V L R I T S L	I K E Q F S T W Q N	200
MbxD	Q D E Q L K L T L K	G H I A E L Q S A R	S Q E Q K L V S V G	A I E H G K T D D	R S L K A E N F I S	247
LktD	Q K T Q K T L A Y R	R K E A E K Q T I F	A Y F R K Y E G A T	R I E Q E K L K D F	K A L Y K Q K S M S	249
ApxID	Q K Y Q K E L A L Q	R E E A E K Q T L	A N I R K Y E G S	R V E N E R L K K D L	K K L F N S K R S T S	249
HlyD	Q K Y Q K E L N L D	E K R A E E L T I L	A R I N Y E N V S	R V E K S R L D D F	R S L L H K Q A I A	250
MbxD	E H A Y L E Q E S K	L I E S N Q N J L Q S	T R S Q W Q K I M A	A I W Q A E W N R M	L Y T Q N L K R D T	297
LktD	R H E L L A Q E N K	L I E A Q N A V A V	Y R S K L N E E N	D L L N V K E E L E	L I T Q F F R S D T	299
ApxID	K H D V U L T Q E N	H I E A V N E L A V	Y K S R L N E E S	D L R Q A K E E I H	L I T Q L F F A D I	299
HlyD	R H A V L E Q E N K	Y K E A A N E L R V	Y K S Q L E P I E S	W I L S A K E E Y Q	L I T Q L F R N M I	300
MbxD	L E S L R Q T N E Q	I N Q I Y T G C T N K	A K Q R Q K L L S I	E S P V N G T Q Q	L T A T T L G G V V	347
LktD	L E K L K Q H I E N	E R Q Q L R L E L E K	N N Q R R Q A S M I	R A P V S G T V Q Q	L K I H T I G G V V	349
ApxID	L E K L K Q N V E A	E K Q Q L S L E L E K	N E Q R Q I A S V I	R A P V S G T V Q Q	L K T H T V G G V V	349
HlyD	L E K L R Q T T S	I E L L T L E L E K	N E R Q Q A S V I	R A P V S G K V Q Q	L K V H T E G G V V	350
MbxD	Q A A E K I M V V A	P N D N Q V E V E V	L V L H K D I G F V	K A G Q N V I I K V	E S F P Y T R Y G Y	397
LktD	T T A E T L M I V	P E D D V L E A T A	L V P H K D I G F V	A A G Q E V I I K V	E T F P Y T R Y G Y	399
ApxID	T T A E T L M V I A	P E D D V L E V T A	L V Q N K D I G F I	E V G Q D A V I K V	E T F P Y T R Y G Y	399
HlyD	T T A E T L M V I V	P E D D T L E V T A	L V Q N K D I G F I	N V G Q N A I I K V	E A F P Y T R Y G Y	400
MbxD	L T G K I K S I S H	D A I E Q H Q L G L	V M T A Z V S F D T	S T L N . I D G V T	I N L T E G M N V T	446
LktD	L T G K I K H I S P	D A I E Q P N V G L	V F N A T I A I D R	K N L T S P D G E K	I D L S S G M T T	449
ApxID	L M G K V K N I T L	D A I E H P Q L G L	V F N S I I S I D R	K T L S G K D G K E	I E L G S G M S V T	449
HlyD	L V G K V R N I N L	D A I E D Q K L G L	V F N V I V S S A E	N D L S T . G N K H	I P L S S G M A V T	449
MbxD	A E I K T G K R R V	E D Y T L S P L I T	K V D E S F R E R	475	SEQ ID NO: 37	
LktD	A E I K T G E R S V	M S Y L L S P L E E	S V T E S L R E R	478	SEQ ID NO: 38	
ApxID	A E I K T G E R S V	I S Y L L S P L E E	S V S E S L R E R	478	SEQ ID NO: 39	
HlyD	A E I K T G M R S V	I S Y L L S P L E E	S V T E S L H E R	478	SEQ ID NO: 40	

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### Cumulative Number of Calves With Severe Ulcers



Number of calves with ulcers with clinical scores >+2

FIG 15

### Number of calves affected each week

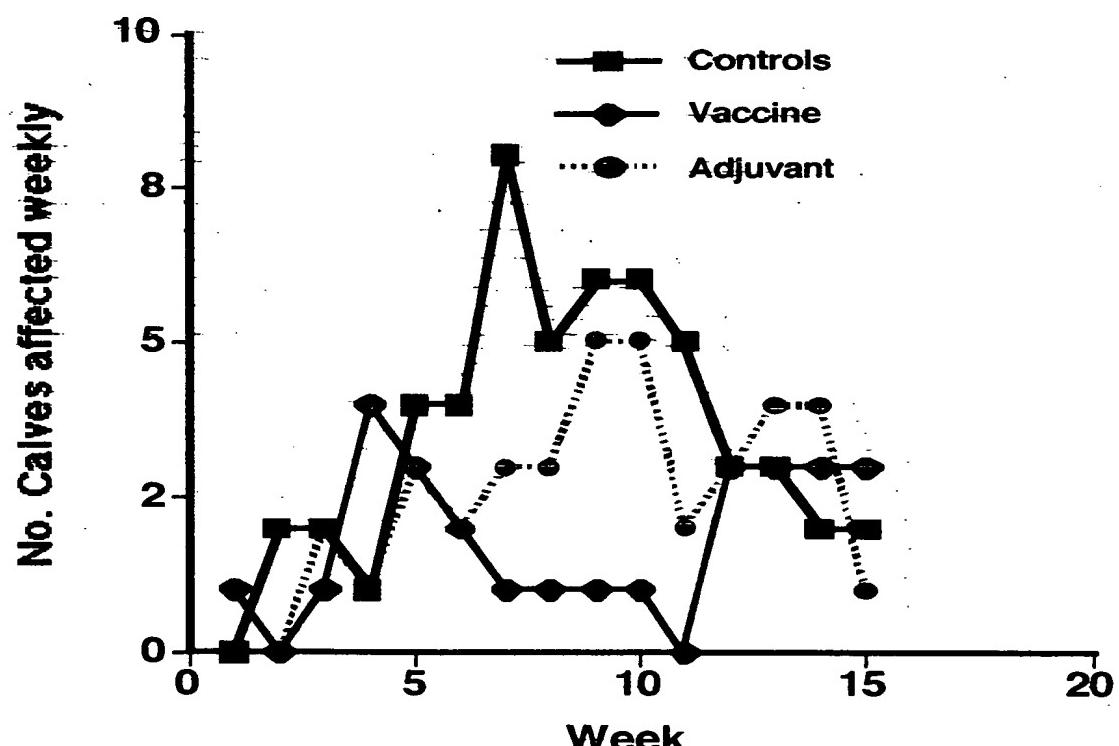
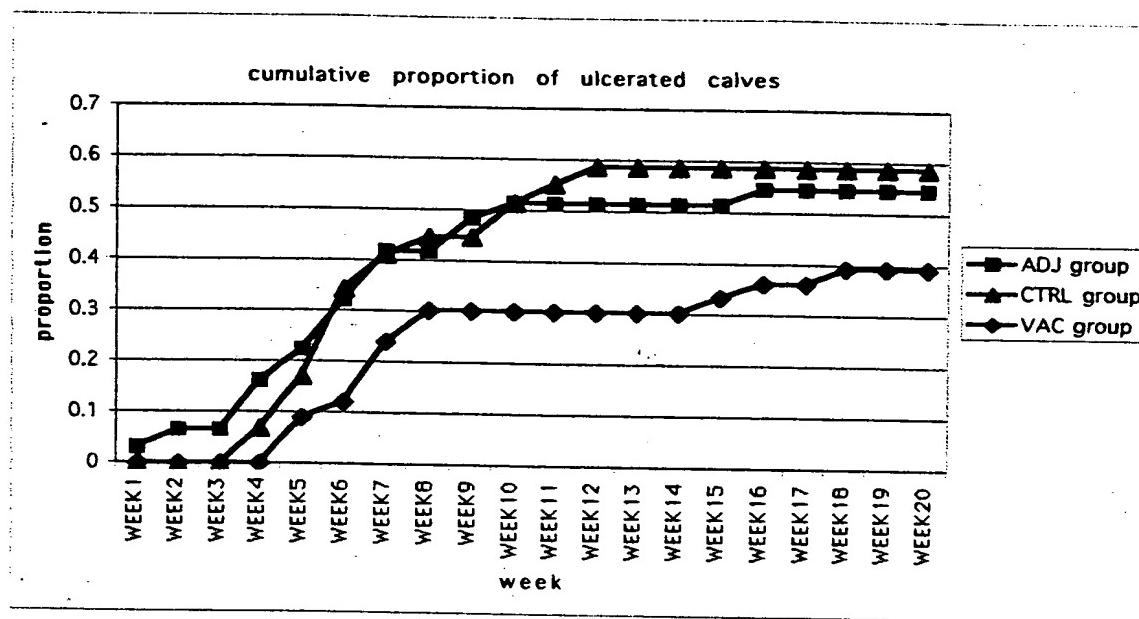


Figure 15

Number of calves affected weekly in 1 group of vaccinated calves and in controls.

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FIG. 16



Cumulative proportion of ulcerated calves during the trial. Calves received as vaccines either saline (designated 'CTRL'), adjuvant alone (designated 'ADJ'), or the recombinant cytotoxin vaccine (designated 'VAC').

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